

10/506455

Re-run

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:

10/506,455

Source:

PLT

Date Processed by STIC:

08/05/2005

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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/506,455

DATE: 08/05/2005

TIME: 10:26:15

Input Set : N:\DA\US10506455.raw

Output Set: N:\CRF4\08042005\J506455.raw

1 <110> APPLICANT: Beals, John
2 Kuchibhotla, Uma
3 <120> TITLE OF INVENTION: HETEROLOGOUS G-CSF FUSION PROTEINS
4 <130> FILE REFERENCE: X-15648
5 <140> CURRENT APPLICATION NUMBER: US/10/506,455
6 <141> CURRENT FILING DATE: 2004-08-31
7 <150> PRIOR APPLICATION NUMBER: PCT/US03/03120
8 <151> PRIOR FILING DATE: 2003-02-21
9 <160> NUMBER OF SEQ ID NOS: 66
10 <170> SOFTWARE: PatentIn version 3.2
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 174
14 <212> TYPE: PRT
15 <213> ORGANISM: Artificial Sequence
16 <220> FEATURE:
17 <223> OTHER INFORMATION: synthetic construct
18 <220> FEATURE:
19 <221> NAME/KEY: MISC_FEATURE
20 <222> LOCATION: (17)..(17)
21 <223> OTHER INFORMATION: Xaa at position 17 is Cys, Ala, Leu, Ser, or Glu;
22 <220> FEATURE:
23 <221> NAME/KEY: MISC_FEATURE
24 <222> LOCATION: (37)..(37)
25 <223> OTHER INFORMATION: Xaa at position 37 is Ala or Asn;
26 <220> FEATURE:
27 <221> NAME/KEY: MISC_FEATURE
28 <222> LOCATION: (38)..(38)
29 <223> OTHER INFORMATION: Xaa at position 38 is Thr, or any other amino acid except Pro;
30 <220> FEATURE:
31 <221> NAME/KEY: MISC_FEATURE
32 <222> LOCATION: (39)..(39)
33 <223> OTHER INFORMATION: Xaa at position 39 is Tyr, Thr, or Ser;
34 <220> FEATURE:
35 <221> NAME/KEY: MISC_FEATURE
36 <222> LOCATION: (57)..(57)
37 <223> OTHER INFORMATION: Xaa at position 57 is Pro or Val;
38 <220> FEATURE:
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40 <222> LOCATION: (58)..(58)
41 <223> OTHER INFORMATION: Xaa at position 58 is Trp or Asn;
42 <220> FEATURE:
43 <221> NAME/KEY: MISC_FEATURE
44 <222> LOCATION: (59)..(59)

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45 <223> OTHER INFORMATION: Xaa at position 59 is Ala or any other amino acid except Pro;
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49 <223> OTHER INFORMATION: Xaa at position 60 is Pro, Thr, Asn, or Ser;
50 <220> FEATURE:
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53 <223> OTHER INFORMATION: Xaa at position 61 is Leu, or any other amino acid except
Pro;
54 <220> FEATURE:
55 <221> NAME/KEY: MISC_FEATURE
56 <222> LOCATION: (62)..(62)
57 <223> OTHER INFORMATION: Xaa at position 62 is Ser or Thr;
58 <220> FEATURE:
59 <221> NAME/KEY: MISC_FEATURE
60 <222> LOCATION: (63)..(63)
61 <223> OTHER INFORMATION: Xaa at position 63 Ser or Asn;
62 <220> FEATURE:
63 <221> NAME/KEY: MISC_FEATURE
64 <222> LOCATION: (64)..(64)
65 <223> OTHER INFORMATION: Xaa at position 64 is Cys or any other amino acid except Pro;
66 <220> FEATURE:
67 <221> NAME/KEY: MISC_FEATURE
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69 <223> OTHER INFORMATION: Xaa at position 65 is Pro, Ser, or Thr;
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73 <223> OTHER INFORMATION: Xaa at position 66 is Ser or Thr;
74 <220> FEATURE:
75 <221> NAME/KEY: MISC_FEATURE
76 <222> LOCATION: (67)..(67)
77 <223> OTHER INFORMATION: Xaa at position 67 is Gln or Asn;
78 <220> FEATURE:
79 <221> NAME/KEY: MISC_FEATURE
80 <222> LOCATION: (68)..(68)
81 <223> OTHER INFORMATION: Xaa at position 68 is Ala or any other amino acid except Pro;
82 <220> FEATURE:
83 <221> NAME/KEY: MISC_FEATURE
84 <222> LOCATION: (69)..(69)
85 <223> OTHER INFORMATION: Xaa at position 69 is Leu, Thr, or Ser;
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88 <222> LOCATION: (93)..(93)
89 <223> OTHER INFORMATION: Xaa at position 93 is Glu or Asn;
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91 <221> NAME/KEY: MISC_FEATURE
92 <222> LOCATION: (94)..(94)
93 <223> OTHER INFORMATION: Xaa at position 94 is Gly or any other amino acid except Pro;

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98 <220> FEATURE:
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100 <222> LOCATION: (97)..(97)
101 <223> OTHER INFORMATION: Xaa at position 97 is Pro, Ser, Thr, or Asn;
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103 <221> NAME/KEY: MISC_FEATURE
104 <222> LOCATION: (133)..(133)
105 <223> OTHER INFORMATION: Xaa at position 133 is Thr or Asn;
106 <220> FEATURE:
107 <221> NAME/KEY: MISC_FEATURE
108 <222> LOCATION: (134)..(134)
109 <223> OTHER INFORMATION: Xaa at position 134 is Gln or any other amino acid except

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Pro:

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117 <223> OTHER INFORMATION: Xaa at position 141 is Ala or Asn;
118 <220> FEATURE:
119 <221> NAME/KEY: MISC_FEATURE
120 <222> LOCATION: (142)..(142)
121 <223> OTHER INFORMATION: Xaa at position 142 is Ser or any other amino acid except

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PRO;

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122 <220> FEATURE:
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124 <222> LOCATION: (143)..(143)
125 <223> OTHER INFORMATION: Xaa at position 143 is Ala, Ser, or Thr.
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127 Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
128 1 5 10 15
129 xaa Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
130 20 25 30
131 Glu Lys Leu Cys Xaa Xaa Xaa Lys Leu Cys His Pro Glu Glu Leu Val
132 35 40 45
133 Leu Leu Gly His Ser Leu Gly Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa
134 50 55 60
135 Xaa Xaa Xaa Xaa Xaa Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
136 65 70 75 80
137 Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Xaa Xaa Xaa Ser
138 85 90 95
139 xaa Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
140 100 105 110
141 Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
142 115 120 125

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143 Ala Leu Gln Pro Xaa Xaa Xaa Ala Met Pro Ala Phe Xaa Xaa Xaa Phe
144 130 135 140
145 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
146 145 150 155 160
147 Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
148 165 170

150 <210> SEQ ID NO: 2
151 <211> LENGTH: 1044
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: synthetic construct
156 <400> SEQUENCE: 2

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| 158 | ggacggctga | gggacggggt | ctcgaaggac | gagttcgct | tagagcaagt | gaggaagatc | 120 |
| 159 | cagggcgatg | gcgcagcgct | ccagcggaat | ctcgttcact | ccttctaggt | cccgtaccg | 180 |
| 160 | cgtcgcgagg | tcgagaagct | gtgtgccacc | tacaagctgt | gccaccccg | ggagctggtg | 240 |
| 161 | ctcttcgaca | cacggtggat | gttcgacacg | gtggggctcc | tcgaccacct | gctcggacac | 300 |
| 162 | tctctgggca | tcccctgggc | tcccctgagc | agctgcgacg | agcctgtgac | agaccgtag | 360 |
| 163 | gggacccgag | gggactcgct | gacgcccagc | caggccctgc | agctggcagg | ctgcttgagc | 420 |
| 164 | caactccata | gcgggtcggt | ccgggacgtc | gaccgtccga | cgaactcggg | tgaggtatcg | 480 |
| 165 | ggccttttcc | tctaccaggg | gctcctgcag | gccctggaag | ggatctcccc | ggaaaaggag | 540 |
| 166 | atggctcccc | aggacgtccg | ggaccttccc | tagaggcccg | agttgggtcc | caccttggac | 600 |
| 167 | acactgcagc | tggacgtcgc | cgacgggctc | aaccacgggt | ggaacctgtg | tgacgtcgac | 660 |
| 168 | ctgcagcggc | tgtttgccac | caccatctgg | cagcagatgg | aagaactggg | aatggccctc | 720 |
| 169 | aaacgggtgg | ggtagaccgt | cgtctacctt | cttgaccctt | accggggagc | cctgcagccc | 780 |
| 170 | aaacagaccc | ccatgccggc | cttcgcctct | gctttccggg | acgtcgggtt | ggtctggcgg | 840 |
| 171 | tacggccgga | agcggagacg | aaagcagcgc | cgggcaggag | gggtcctggt | tgctcccat | 900 |
| 172 | ctgcagagct | tcgtcgcggc | cgtcctccc | caggaccaac | ggagggtaga | cgtctcgaag | 960 |
| 173 | ctggaggtgt | cgtaccgcgt | cttaaggcac | cttgcccagc | ccgacctcca | cagcatggcg | 1020 |
| 174 | cagaattccg | tggaacgggt | cggg | | | | 1044 |

176 <210> SEQ ID NO: 3
177 <211> LENGTH: 1044
178 <212> TYPE: DNA
179 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: synthetic construct
182 <400> SEQUENCE: 3

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|-----|------------|------------|------------|------------|------------|------------|-----|
| 183 | acccccctgg | gccctgccag | ctccctgccc | cagagcttcc | tgctcaagt | gggggacccg | 60 |
| 184 | ggacggctga | gggacggggt | ctcgaaggac | gagttcgct | tagagcaagt | gaggaagatc | 120 |
| 185 | cagggcgatg | gcgcagcgct | ccagcggaat | ctcgttcact | ccttctaggt | cccgtaccg | 180 |
| 186 | cgtcgcgagg | tcgagaagct | gtgtgccacc | tacaagctgt | gccaccccg | ggagctggtg | 240 |
| 187 | ctcttcgaca | cacggtggat | gttcgacacg | gtggggctcc | tcgaccacct | gctcggacac | 300 |
| 188 | tctctgggca | tcccctgggc | tcccctgagc | agctgcgacg | agcctgtgac | agaccgtag | 360 |
| 189 | gggacccgag | gggactcgct | gacgcccagc | caggccctgc | agctggcagg | ctgcttgagc | 420 |
| 190 | caactccata | gcgggtcggt | ccgggacgtc | gaccgtccga | cgaactcggg | tgaggtatcg | 480 |
| 191 | ggccttttcc | tctaccaggg | gctcctgcag | gccctggaag | ggatctcccc | ggaaaaggag | 540 |
| 192 | atggctcccc | aggacgtccg | ggaccttccc | tagaggcccg | agttgggtcc | caccttggac | 600 |
| 193 | acactgcagc | tggacgtcgc | cgacgggctc | aaccacgggt | ggaacctgtg | tgacgtcgac | 660 |

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Input Set : N:\DA\US10506455.raw

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194      ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggccctt 720
195      aaacgggtgg ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc 780
196      acccaggggtg ccatgccggc cttcaactct accttcggg acgtcgggtg ggteccacgg 840
197      tacggccgga agttgagatg gaagcagcgc cgggcaggag gggtcctggg tgcctcccat 900
198      ctgcagagct tcgtcgcggc cgtctctccc caggaccaac ggagggtaga cgtctcgaag 960
199      ctggaggtgt cgtaccgcgt ctttaaggcac cttgcccagc ccgacctcca cagcatggcg 1020
200      cagaattccg tggaaacggg cggg                                     1044
202 <210> SEQ ID NO: 4
203 <211> LENGTH: 1044
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: synthetic construct
208 <400> SEQUENCE: 4
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211      cagggcgatg gcgcagcgtt ccagcggaat ctcgttcact ccttctaggt cccgctaccg 180
212      cgtcgcgagg tcgagaagct gtgttaacac accaagctgt gccaccccgga ggagctgggtg 240
213      ctcttcgaca cattgtgggt gtctgcacac gtggggctcc tcgaccacct gctcggacac 300
214      tctctgggca tcccctgggc tcccctgagc agctgcgacg agcctgtgac agacccgtag 360
215      gggacccgag gggactcgtc gacgcccagc caggccctgc agctggcagg ctgcttgagc 420
216      caactccata gcgggtcggg ccgggacgtc gaccgtccga cgaactcggg tgaggtatcg 480
217      ggcccttttc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag 540
218      atgggtcccc aggacgtccg ggaccttccc tagaggcccg agttgggtcc caccttggac 600
219      aactgcagc tggacgtcgc cgacgggctc aaccaggggt ggaacctgtg tgacgtcgac 660
220      ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggccctt 720
221      aaacgggtgg ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc 780
222      acccaggggtg ccatgccggc cttcgcctct gctttccggg acgtcgggtg ggtccacagg 840
223      tacggccgga agcggagacg aaagcagcgc cgggcaggag gggtcctggg tgcctcccat 900
224      ctgcagagct tcgtcgcggc cgtctctccc caggaccaac ggagggtaga cgtctcgaag 960
225      ctggaggtgt cgtaccgcgt ctttaaggcac cttgcccagc ccgacctcca cagcatggcg 1020
226      cagaattccg tggaaacggg cggg                                     1044
228 <210> SEQ ID NO: 5
229 <211> LENGTH: 1044
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: synthetic construct
234 <400> SEQUENCE: 5
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237      cagggcgatg gcgcagcgtt ccagcggaat ctcgttcact ccttctaggt cccgctaccg 180
238      cgtcgcgagg tcgagaagct gtgtgccacc tacaagctgt gccaccccgga ggagctgggtg 240
239      ctcttcgaca caggggtgat gtctgcacac gtggggctcc tcgaccacct gctcggacac 300
240      tctctgggca tcccctgggc taacactagc agctgcgacg agcctgtgac agacccgtag 360
241      gggacccgat tggactcctc gacgcccagc caggccctgc agctggcagg ctgcttgagc 420
242      caactccata gcgggtcggg ccgggacgtc gaccgtccga cgaactcggg tgaggtatcg 480
243      ggcccttttc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag 540
244      atgggtcccc aggacgtccg ggaccttccc tagaggcccg agttgggtcc caccttggac 600
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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/506,455

DATE: 08/05/2005
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Input Set : N:\DA\US10506455.raw
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 17,37,38,39,57,58,59,60,61,62,63,64,65,66,67,68,69,93,94

Seq#:1; Xaa Pos. 95,97,133,134,135,141,142,143

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 29,45,53,65,81,93,109,121

VERIFICATION SUMMARY

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Input Set : N:\DA\US10506455.raw

Output Set: N:\CRF4\08042005\J506455.raw

L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16
M:341 Repeated in SeqNo=1